

**AMENDMENTS TO THE SPECIFICATION**

Please amend the paragraph beginning on line 5 of page 15 as follows:

--Once an accessible region is identified, a search for a target site can be conducted within the nucleotide sequence of the accessible region. For exogenous molecules which do not have binding specificity, or which exhibit a relaxed or promiscuous specificity, it may not be necessary to identify a target site. Exogenous molecules such as proteins and, in particular, transcription factors, often have a preferred target site. In these cases, the nucleotide sequence of the accessible region can be searched for the presence of the preferred target site. Target sites for various transcription factors are known. *See, for example, Wingender et al. (1997) Nucleic Acids Res. 25:265-268 and the TRANSFAC Transcription Factor database, available on the Internet and at <http://transfac.gbf.de/TRANSFAC/>, accessed on April 13, 2000.* In general, target sites for newly-discovered transcription factors, as well as other types of exogenous molecule, can be determined by methods that are well-known to those of skill in the art such as, for example, electrophoretic mobility shift assay, exonuclease protection, DNase footprinting, chemical footprinting and/or direct nucleotide sequence determination of a binding site. *See, for example, Ausubel et al., supra, Chapter 12.*